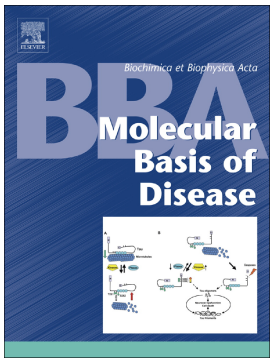


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# Systematic Identification of Rabbit LncRNAs Reveals Functional Roles in Atherosclerosis

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## Abstract

Long noncoding RNAs (lncRNAs) have been gradually emerging as important regulators in various biological processes and diseases, while the contributions of lncRNAs to atherosclerosis remain largely unknown. Our previous work has discovered atherosclerosis associated protein-coding genes by transcriptome sequencing of rabbit models. Here we investigated the roles of lncRNAs in atherosclerosis. We defined a stringent set of 3,736 multi-exonic lncRNA transcripts in rabbits. All lncRNAs are firstly reported and 609 (16.3%) of them are conserved in 13 species. Rabbit lncRNAs have similar characteristics to lncRNAs in other mammals, such as relatively short length, low expression, and highly tissue-specificity. The integrative analysis of lncRNAs and co-expressed genes characterize diverse functions of lncRNAs. Comparing two kinds of atherosclerosis models (LDLR-deficient WHHL rabbits and cholesterol-fed NZW rabbits) with their corresponding controls, we found the expression changes of two rabbit models were similar in aorta in but different in liver. The shared change in aorta revealed a subset of lncRNAs involved in immune response, while the cholesterol-fed NZW rabbits showed broader lncRNA expression changes in skeletal muscle system compared to WHHL rabbits. These atherosclerosis-associated lncRNAs and genes provide hits for the experimental validation of lncRNA functions. In summary, our study systematically identified rabbit lncRNAs for the first time and provides new insights for understanding the functions of lncRNAs in atherosclerosis.